

PCT-AU00-00864 Amended Sequence Listing.txt
SEQUENCE LISTING

<110> St Vincent's Institute of Medical Research
<120> Inhibitor of Osteoclast Precursor Formation
<130> FP13129
<140> PCT/AU00/00864
<141> 2000-07-19
<150> AU PQ1675
<151> 1999-07-19
<160> 66
<170> PatentIn version 3.3
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<213> Artificial
<220>
<223> sense primer complementary to rat calcitonin cDNA
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<212> DNA
<213> Rattus rattus
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<212> DNA

<213> Rattus rattus

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<211> 22

<212> DNA

<213> Artificial

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<223> sense specific primer complementary to SEQ ID NO:4

<400> 5

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<211> 25

<212> DNA

<213> Artificial

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<223> sense specific primer complementary to SEQ ID NO:4

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<210> 7

<211> 1302

<212> DNA

<213> Rattus rattus

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 <212> DNA
 <213> Rattus rattus

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<211> 620
<212> DNA
<213> Rattus rattus

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<212> DNA
<213> Mus musculus

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 <211> 9862
 <212> DNA
 <213> Mus musculus

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 <222> (636)..(636)
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PCT-AU00-00864 Amended Sequence Listing.txt

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PCT-AU00-00864 Amended Sequence Listing.txt

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<220>
 <223> antisense to C-type lectin region of OCIL

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<220>
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PCT-AU00-00864 Amended Sequence Listing.txt

<400> 23
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<210> 24
<211> 21
<212> DNA
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<220>
<223> antisense to sequence upstream of open reading frame of OCIL

<400> 24
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<210> 25
<211> 20
<212> DNA
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<220>
<223> antisense to sequence in open reading frame of OCIL but outside C-type lectin region

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<220>
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Leu Asn Phe

<210> 27
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<220>
<223> sense primer

<400> 27
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<210> 28
<211> 31
<212> DNA
<213> Artificial

PCT-AU00-00864 Amended Sequence Listing.txt

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<223> antisense primer

<400> 28

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31

<210> 29

<211> 633

<212> DNA

<213> Mus musculus

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<213> Artificial

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<223> sense primer

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<210> 31

<211> 28

<212> DNA

<213> Artificial

<220>

<223> antisense primer

<400> 31

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28

<210> 32

<211> 28

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<212> DNA
<213> Artificial

<220>
<223> antisense primer

<400> 32
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28

<210> 33
<211> 1628
<212> DNA
<213> Rattus rattus

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aaaaaaaa	1628

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 <213> Artificial

<220>
 <223> antisense primer

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<210> 35
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> sense specific primer

<400> 35	
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<210> 36
 <211> 1206
 <212> DNA
 <213> Mus musculus

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 <222> (332)..(332)
 <223> n is a, c, g, or t

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35 40 45

Ile Met Val Leu Thr Val Ala Val Ile Ala Leu Ser Val Ala Leu Ser
50 55 60

Ala Thr Lys Thr Glu Gln Ile Pro Val Asn Lys Thr Tyr Ala Ala Cys
65 70 75 80

Pro Gln Asn Trp Ile Gly Val Glu Asn Lys Cys Phe Tyr Phe Ser Glu
Page 30

Tyr Pro Ser Asn Trp Thr Phe Ala Gln Ala Phe Cys Met Ala Gln Glu
100 105 110

Ala Gln Leu Ala Arg Phe Asp Asn Gln Asp Glu Leu Asn Phe Leu Met
115 120 125

Arg Tyr Lys Ala Asn Phe Asp Ser Trp Ile Gly Leu His Arg Glu Ser
130 135 140

Ser Glu His Pro Trp Lys Trp Thr Asp Asn Thr Glu Tyr Asn Asn Thr
145 150 155 160

Ile Pro Ile Arg Gly Glu Glu Arg Phe Ala Tyr Leu Asn Asn Asn Gly
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Ile Ser Ser Thr Arg Ile Tyr Ser Leu Arg Met Trp Ile Cys Ser Lys
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35 40 45

Glu Ser Ser Ala Lys Leu Tyr Cys Cys Tyr Gly Val Ile Met Val Leu
50 55 60

Thr Val Ala Val Val Ala Leu Ser Val Ala Leu Ser Val Thr Lys Thr
65 70 75 80

Glu Gln Ile Leu Ile Asn Lys Thr Tyr Ala Ala Cys Pro Lys Asn Trp
85 90 95

Ile Gly Val Gly Asn Lys Cys Phe Tyr Phe Ser Glu Tyr Thr Ser Asn
Page 31

100

105

110

Trp Thr Phe Ala Gln Thr Phe Cys Met Ala Gln Glu Ala Gln Leu Ala
 115 120 125

Arg Phe Asp Asn Glu Lys Glu Leu Asn Phe Leu Met Arg Tyr Lys Ala
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Asn Phe Asp Ser Trp Ile Gly Leu His Arg Glu Ser Ser Glu His Pro
 145 150 155 160

Trp Lys Trp Thr Asp Asn Thr Glu Tyr Asn Asn Met Ile Pro Ile Gln
 165 170 175

Gly Val Glu Thr Cys Ala Tyr Leu Ser Gly Asn Gly Ile Ser Ser Ser
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Ser Leu His Cys Pro Thr Pro Val Pro Val
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 35 40 45

Val Ser Pro Val Lys Leu Tyr Cys Cys Tyr Gly Val Ile Met Val Leu
 50 55 60

Thr Val Ala Val Ile Ala Leu Ser Val Ala Leu Ser Thr Lys Lys Thr
 65 70 75 80

Glu Gln Ile Ile Ile Asn Lys Thr Tyr Ala Ala Cys Ser Lys Asn Trp
 85 90 95

Thr Gly Val Gly Asn Lys Cys Phe Tyr Phe Ser Gly Tyr Pro Arg Asn
 Page 32

100

105

110

Trp Thr Phe Ala Gln Ala Phe Cys Met Ala Gln Glu Ala Gln Leu Ala
 115 120 125

Arg Phe Asp Asn Glu Glu Glu Leu Ile Phe Leu Lys Arg Phe Lys Gly
 130 135 140

Asp Phe Asp Cys Trp Ile Gly Leu His Arg Glu Ser Ser Glu His Pro
 145 150 155 160

Trp Lys Trp Thr Asn Asn Thr Glu Tyr Asn Asn Met Asn Pro Ile Leu
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Gly Val Gly Arg Tyr Ala Tyr Leu Ser Ser Asp Arg Ile Ser Ser Ser
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Asn Leu His Cys Gln Thr Pro Pro Val
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PCT-AU00-00864 Amended Sequence Listing.txt

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Gln Glu

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<220>
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<210> 59
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<220>
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PCT-AU00-00864 Amended Sequence Listing.txt 22
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 <223> lambda_gt11 reverse primer

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<210> 61
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> sense primer

<400> 61
 tgagtgtgag gaaggcggtt ac 22

<210> 62
 <211> 20
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 <213> Artificial

<220>
 <223> antisense primer

<400> 62
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<210> 63
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> sense primer

<400> 63
 accaaagtga atgccgag 18

<210> 64
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> 5' primer

<400> 64
 catggagaag gctggggctc 20

PCT-AU00-00864 Amended Sequence Listing.txt

<210> 65
<211> 20
<212> DNA
<213> Artificial

<220>
<223> 3' primer

<400> 65
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20

<210> 66
<211> 20
<212> DNA
<213> Artificial

<220>
<223> sense primer

<400> 66
gctgtgggca aggtcatccc

20



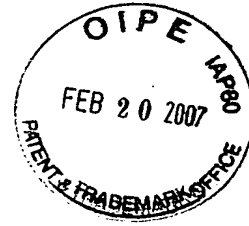
containing a 721 bp fragment were obtained from three sources, ST2 mouse stromal cells, primary mouse calvarial osteoblasts and mouse liver tissue. In 2 of the 7 clones, there was 100% identity to mOCILrPI sequence, and 92.2% identity to mOCIL after the first 115 bp. In the other 5 clones, when compared to the mOCILrPI sequence, there was 100% identity in the first 106 bp (exons I and II), but only 90.5% identity in the remaining 615 bp. This 721 bp fragment, originally designated as mOCIL47, was redesignated as mOCILrP2 (SEQ ID NO: 15). MOCILrP2 is related to, but distinct from, mOCIL (SEQ ID NO: 36) and mOCILrPI (SEQ ID NO: 12).

A sense primer representing nucleotides 343-364 of mOCIL2kb (SEQ ID NO: 10) and representing nucleotides 34-57 of mOCIL (SEQ ID NO: 36), designated as OCILml7 (SEQ ID NO: 16),

OCILml7 5'-TGG AAA CTC AGC TCC TCA GCT CTG-3'

and antisense primer OCILml2 were also used to carry out RT-PCR with RNA from three sources, ST2 mouse stromal cells, primary mouse calvarial osteoblasts and mouse liver tissue, as above. PCR was run under the same conditions as above. Ten clones were obtained, each containing a 713 bp fragment. This sequence is designated mOCIL17 (SEQ ID NO: 17), and is ~~100%~~ identical to mOCIL (SEQ ID NO: 36); 1206 base pairs, from nucleotides 34 to 74 of SEQ ID NO: 36, except that the base at position 730 in SEQ ID NO: 36 is C, whereas the corresponding base is T at position 707 in SEQ ID NO: 17.

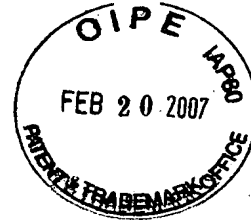
RT-PCR was also carried out using a sense primer corresponding to the region located at the junction of exons II and III, representing nucleotides 245-269 of mOCIL



(SEQ ID NO: 36) and at the junction of exon III and exon IV, representing nucleotides 243-267 of mOCILrPI (SEQ ID NO: 12), and designated primer OCILm32 (SEQ ID NO: 18),

5 OCILm32 5'-TTT GTC AGC AAC AAA GAC AGA ACA G-3'

The primer oligonucleotide OCILm32 has 23 of 24 bp complementary to mOCILrPI:



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